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Patent

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Plant GntI sequences and the use thereof for the production
of plants having reduced or lacking N-acetyl glucosaminyl
transferase I (GnTI) activity

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The present invention relates to plant GnTI sequences, in particular, plant nucleic acid sequences encoding the enzyme N-acetyl glucosaminyl transferase I (GnTI), as well as *GntI* antisense or sense constructs, deduced therefrom, and their translation products, antibodies directed against said translation products as well as the use of the sequence information for the production of transformed microorganisms and of transgenic plants, including those with reduced or lacking N-acetyl glucosaminyl transferase I activity. Such plants with reduced or lacking N-acetyl glucosaminyl transferase I activity are of great importance for the production of glycoproteins of specific constitution with respect to their sugar residues.

Prior art:

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In eukaryotes, glycoproteins are cotranslationally assembled in the endoplasmatic reticulum (ER) (i.e. during import into the ER lumen) by the attachment of initially membrane bound glycans (via dolichol pyrophosphate) to specific asparagine residues in the growing polypeptide chain (N-glycosylation). In higher organisms, sugar units located at the surface of the folded polypeptide chain are subjected to further trimming and modification reactions (ref. 1) in the Golgi cisternae. Initially, typical basic $\text{Glc}_3\text{Man}_9\text{GlcNAc}_2$ units of the high-mannose type are formed by means of different glycosidases and glycosyl transferases in the ER, which during the passage through the different Golgi cisternae are subsequently converted to so-called complex glycans. The latter are characterized by less mannose units and the presence of

additional sugar residues, such as fucose, galactose and/or xylose in plants and sialic acid (N-acetyl neuraminic acid, NeuNAc) in mammals (ref. 1,2,3). The extent of the modifications can differ between glycoproteins. Single polypeptide chains may carry heterogeneous sugar chains. Furthermore, the glycosylation pattern may vary for a specific polypeptide (tissue specific differences), and does not always have to be uniform with respect to a specific glycosylation site, which is referred to as microheterogeneity (ref. 4,5). Up to now, the role of asparagine bound glycans is barely understood, which i.a. results from the fact, that said glycans may serve several functions (ref. 6). However, it can be assumed, that e.g. protection of a polypeptide chain from proteolytic degradation can also be achieved by glycans of a more simple oligomannosyl type (ref.7).

Description of problems:

Glycoproteins are highly important in medicine and research. However, large scale isolation of glycoproteins is time-consuming and expensive. The direct use of glycoproteins isolated conventionally often raises problems, since upon administration as a therapeutic, single residues of the glycan components may cause undesired side effects. In this context, the glycan component predominantly contributes to the physico-chemical properties (such as folding, stability and solubility) of the glycoproteins. Furthermore, isolated glycoproteins, as already mentioned above, rarely carry uniform sugar residues, which is referred to as microheterogeneity.

For the production of glycoproteins for medicine and research, yeasts prove to be unsuitable, since they are only able to perform glycosylations of the so-called high-mannose type. While insects and higher plants exhibit complex glycoprotein modifications, these, however, differ from those of animals. Therefore, glycoproteins isolated from plants have a strong antigenic effect in mammals. In most cases, animal organisms

with glycosylation defects are not viable, since terminal glycan residues (e.g. of membraneous glycoproteins) mostly possess biological signal function and are indispensable for cell-cell-recognition during the course of embryogenesis. Mammalian cell lines with defined glycosylation defects already exist, the cultivation of which, however, is labour-intensive and expensive.

For mammals, different glycosylation mutants have been described in detail at the cell culture level (ref. 7,8,9,10). Said mutants are either defective in biosynthesis of mature oligosaccharide chains attached to dolichol pyrophosphate or in glycan processing or show alterations in their terminal sugar residues, respectively. Some of these cell lines exhibit a conditional-lethal phenotype or are defective in intracellular protein transport. The consequences of said defects for the intact organism are difficult to estimate. It has been observed, that a modification in the pattern of complex glycans on the cell surfaces of mammals is accompanied by the formation of tumours and metastases, although a functional relationship could not yet unambiguously be demonstrated (ref. 9). Therefore, in mammals glycosylation mutants are very rare. These defects, summarized under HEMPAS (Hereditary Erythroblastic Multinuclearity with a Positive Acidified Serum lysis test) (ref. 10,11), are based either on a deficiency in mannosidase II and/or low levels of the enzyme N-acetyl glucosaminyl transferase II (GnTII), and have strongly limiting effects on the viability of the mutated organism. *GntI* knock-out mice, in which the gene for GnTI has been destroyed, already die in utero of multiple developmental defects (personal communication, H. Schachter, Toronto).

Until recently, no comparable mutants were known for plants. By the use of an antiserum, which specifically recognizes complex modified glycan chains of plant glycoproteins and which predominantly is directed against the highly antigenic

β 1 \rightarrow 2 linked xylose residues (ref. 12), the applicant was able to isolate several independent mutants from an EMS mutagenized F2 population of the genetic model plant *Arabidopsis thaliana*, which no longer showed complex glycoprotein modification (complex glycan, *cgl* mutants). After at least five backcrosses, each followed by intermittent selfings (to screen for the recessive defects), the glycoproteins were analyzed. These glycoproteins mainly carried glycans of the Man₅GlcNAc₂ type, indicating a defect in N-acetyl glucosaminyl transferase I (GnTI) (ref. 8). Indeed, the *Arabidopsis cgl* mutants lacked GnTI activity (ref. 13), which normally catalyzes the first reaction in the synthetic pathway to complex modified sugar chains (ref. 1). However, according to observations so far, the viability of the mutated plants is not affected. In recent publications, plants are suggested as a putative source for the production of pharmaceutically relevant glycoproteins or vaccines (ref. 14,15). There however, it was overlooked, that glycoproteins isolated from plants may cause severe immune reactions in mammals, which up to now obstructed the production of heterologous glycoproteins in cultivated plants.

The applicant could demonstrate by way of example for the *Arabidopsis cgl* mutant, that plants can manage without complex modified glycoproteins to a great extent (ref. 13). Initially, secretory proteins are normally glycosylated in the ER of the mutant. In the Golgi apparatus of the *cgl* mutant, however, the oligomannosyl chains linked to the polypeptide backbone via asparagine residues (N-glycosylation) then remain at the stage of Man₅GlcNAc₂ residues, since N-acetyl glucosaminyl transferase I (GnTI) activity is missing (Fig. 1). By this biosynthesis block, the plant specific complex glycoprotein modification and in particular the attachment of α 1 \rightarrow 3 fucose and β 1 \rightarrow 2 xylose residues is prevented, whereby the strong antigenic effect on the mammalian organism is absent. However, *Arabidopsis* as a herb only has little utilizable biomass. Therefore, for the large scale production of biotechnologically relevant glycoproteins these *cgl* plants are less

suitable. As an alternative, cultivars, especially Solanaceae, such as potato, tobacco, tomato or pepper and furthermore alfalfa, canola, beets, soybean, lettuce, corn, rice and grain, with missing or highly reduced GntI activity, would be ideal for the production of heterologous glycoproteins in plants. For this purpose, the methods of homology-dependent gene silencing would be applicable (ref. 16, 17).

As Fig. 3 demonstrates, the homology of the first determined plant *GntI* sequence from potato (*Solanum tuberosum* L., St) is extraordinary low in comparison to the corresponding known sequences of animal organisms (only 30-40% identity at the protein level, cf. Fig. 3A). Therefore, by the use of heterologous *GntI* gene sequences an efficient reduction of endogenous complex glycoprotein modification in plants by means of antisense or sense suppression, respectively, (ref. 21), probably cannot be achieved.

Thus, in medicine and research there is still the need for a cost-effective production in suitable organisms of recombinant glycoproteins with a minimum of uniform, i.e. defined sugar residues.

Nature of the present invention:

Since the applicant for the first time has been able to isolate and elucidate plant *GntI* cDNA sequences, it is now possible i.a. to obtain and, in particular, to generate any plant having reduced or missing GntI activity, and to detect the corresponding mutants, respectively, by means of reverse genetic approaches following transposon (ref. 18) or T-DNA insertion (ref. 19), respectively, so as to produce glycoproteins with low antigenic potential in said mutants.

i) Enzymes

Generally, the present invention comprises different N-acetyl glucosaminyl transferase I enzymes (EC 2.4.1.101) from plants, e.g. potato (*Solanum tuberosum* L.), tobacco (*Nicotiana tabacum* L.) and *Arabidopsis thaliana* (L.). In particular, the present invention relates to enzymes, which exhibit or contain the amino acid sequences given in Fig. 2 and 3B as well as in the accompanying sequence protocol.

Further, the invention comprises enzymes, which are derived from amino acid sequences of the above mentioned enzymes by amino acid substitution, deletion, insertion, modification or by C-terminal and/or N-terminal truncation and/or extension, and which - if showing enzymatic activity - exhibit a specificity comparable to that of the starting enzyme, i.e. N-acetyl glucosaminyl transferase I activity, and optionally a comparable activity.

In the present context, by the term "comparable activity" an activity is understood, which is in the range of up to 100% above or below that of the starting enzyme. Accordingly, also comprised by the invention are derived enzymes or proteins with very low or completely lacking enzymatic activity, which is detectable by means of one or more of the tests mentioned as follows. The enzyme activity is determined by a standard assay, which is performed with microsomal fractions either under radioactive conditions, e.g. using UDP-[6-³H]GlcNAc as a substrate (ref. 13) or non-radioactive conditions (HPLC method; ref 20). Plant GnTI activity can be detected on the subcellular level in Golgi fractions (ref. 21). On account of low yields, however, it is almost impossible to enrich the enzyme from plants.

Alternatively, an enzyme derived according to the present invention, may optionally be defined as an enzyme, for which a DNA sequence encoding the enzyme can be determined or

derived, which hybridizes to a DNA sequence encoding the starting enzyme or to a complementary sequence under stringent conditions, as defined as follows.

For example, an enzyme derived in such a manner represents an isoform, which comprises the amino acids 74 to 446 of the amino acid sequence illustrated in Fig. 2 and in SEQ ID No:1 and 2. This isoform *i.a.* lacks the membrane anchor formed by amino acids 10 to 29. As a result, this enzyme isoform may be located in the plant cytosol.

As examples for C- and/or N-terminally extended proteins, fusion proteins can be mentioned, comprising in addition to an amino acid sequence according to the invention a further protein, which e.g. exhibits a different enzymatic activity or which may be easily detected in another manner, such as by means of fluorescence or phosphorescence or on account of a reactivity with specific antibodies or by binding to suitable affinity matrices.

Furthermore, the invention comprises fragments of said enzymes, which optionally no longer exhibit any enzymatic activity. Generally, these fragments show an antigenic effect in a host immunized with said fragments, and may accordingly be employed as an antigen for the production of monoclonal or polyclonal antibodies by immunization of a host with those fragments.

Moreover, this invention also relates to N-acetyl glucosaminyl transferase I enzymes from other varieties and plant species, which are obtainable on account of hybridization of their genes or one or more regions of their genes:

- to one or more of the DNA sequences and/or DNA fragments of the present invention, as discussed below and/or
- to suitable hybridization probes according to the invention, which may be prepared on the basis of the amino acid sequences mentioned in the sequence protocol considering the degeneration of the genetic code.

Further comprised by the invention in accordance with the above are enzymes or proteins derived from these N-acetyl glucosaminyl transferase I enzymes, including fusion proteins thereof, as well as fragments of all of these enzymes or proteins.

ii) Antibodies

Another aspect of the present invention relates to the use of the amino acid sequences mentioned above and of fragments thereof having antigenic effects, respectively, for the production of monoclonal or polyclonal antibodies or antisera by immunizing hosts with said amino acid sequences or fragments, respectively, as well as of antibodies or antisera, respectively, *per se*, which specifically recognize and bind to the enzymes and/or antigens described above. The general procedure and the corresponding techniques for the generation of polyclonal and monoclonal antibodies are all well-known to the persons skilled in the art.

Exemplarily, by the use of a fragment of the *GntI* cDNA (nucleotides 275 to 1395) represented in Fig. 2 and SEQ ID NO: 1, the recombinant GntI protein from *Solanum tuberosum* with 10 N-terminal histidine residues (His-tag) was overexpressed in *E. coli*, and, following affinity purification via a metal-chelate matrix, was employed as an antigen for the production of polyclonal antisera in rabbits (cf. Examples 5 and 6).

One possible use of the antibodies of the invention resides in the screening of plants for the presence of N-acetyl glucosaminyl transferase I.

Binding of the antibody according to the present invention to plant protein(s) indicates the presence of N-acetyl glucosaminyl transferase I enzyme detectable with said antibody. In

general, this antibody may then be covalently bound to a carrier in a later step, and optionally be employed for the enrichment or purification of the enzyme by means of column chromatography.

5 On the other hand, a negative binding result using the antibody of the present invention, i.e. lack of binding to the plant proteins, may suggest, that N-acetyl glucosaminyl transferase I enzyme is absent (or highly modified by muta-
10 tion), and thus, that N-acetyl glucosaminyl transferase I activity of a plant investigated is missing or highly reduced.

15 Techniques for the realization of the screening assays mentioned above or the enrichment or purification of enzymes by the use of antibody columns or other affinity matrices (cf. Examples 5 and 6) are well-known to those skilled in the art.

20 iii) DNA sequences

The present invention further comprises DNA sequences encoding the amino acid sequences of the invention, including
25 amino acid sequences derived therefrom according to the above provisions. In particular, the invention relates to the respective gene, which is the basis of the amino acid sequences described in the Figures 2 and 3B and the sequence protocol, and especially, to the cDNA sequences described in Fig.
30 2 and the sequence protocol, as well as to DNA sequences derived from these genes and DNA sequences.

35 By the term "derived DNA sequences" are meant sequences, which are obtained by substitution, deletion and/or insertion of one or more and/or smaller groups of nucleotides of the sequences mentioned above and/or by truncation or extension
40 at the 5' and/or 3' terminus. Modifications within the DNA sequence may lead to derived DNA sequences, which encode amino acid sequences being identical to the amino acid sequence encoded by the starting DNA sequence, or to such

sequences, in which, compared to the amino acid sequence, which is encoded by the starting DNA sequence, single or a few amino acids are altered, i.e. substituted, deleted and/or inserted, as well as to such sequences, which - optionally in addition - are truncated and/or extended at the C-terminus and/or N-terminus.

Furthermore, the present invention also extends to the complementary sequences of the genes and DNA sequences according to the invention, as well as the RNA transcription products thereof.

Particularly comprised by the present invention are all sequences derived according to the above provisions, which over their entire length or only with one or more partial regions hybridize under stringent conditions to the starting sequences mentioned above or to the sequences complementary thereto or to parts thereof, as well as DNA sequences comprising such sequences.

By the term "hybridization under stringent conditions" in the sense of the present invention is understood a hybridization procedure according to one or more of the methods described below. Hybridizing: up to 20 h in PEG buffer according to Church and Gilbert (0.25 M Na_2HPO_4 , 1mM EDTA, 1% (w/v) BSA, 7% (w/v) SDS, pH 7.5 with phosphoric acid; ref. 22) at 42°C or in standard hybridization buffers with formamide at 42°C or without formamide at 68°C (ref. 23). Washing: 3 times at 65°C for 30 min in 3x SSC-buffer (ref. 23), 0.1% SDS.

In the sense of the present application, the term "hybridization" always means hybridization under stringent conditions, as mentioned above, even if this is not explicitly indicated in the individual case.

Moreover, the invention relates to fragments of the DNA sequences mentioned above, including the DNA sequences

derived in accordance with the above provisions, to fragments derived from such fragments by nucleic acid substitution, insertion and/or deletion as well as the corresponding fragments with sequences complementary thereto. Such fragments are *i.a.* suitable as sequencing or PCR primers, screening probes and/or for uses as discussed below. For the use as a screening or hybridizing probe, the DNA fragments according to the present invention are frequently employed as radio-labelled fragments. Fragments carrying sequences, which are derived from the starting sequences defined above by substitution, deletion and/or insertion of one or more nucleotides, and the sequences complementary thereto, respectively, are comprised by the invention to that extent, as said fragments hybridize under the above mentioned stringent conditions to the starting sequences, or to the sequences complementary thereto, respectively.

On the basis of the DNA sequences mentioned in the sequence protocol and in Figure 2, DNA fragments according to the invention may for example be obtained starting from plant DNA by means of restriction endonucleases using appropriate restriction sites or by employment of PCR by means of primers appropriately synthesized, or may, as an alternative, also be chemically synthesized. Such techniques are well-known to those skilled in the art.

Moreover, the invention relates to any DNA sequences, which represent a gene or are a part of a gene encoding the enzyme N-acetyl glucosaminyl transferase I and, which in their entirety or in a partial region thereof hybridize under stringent conditions

- to one or more of the DNA sequences of the invention and/or
- to one or more of the DNA fragments of the invention and/or
- to a DNA sequence, which is derived from the amino acid sequences mentioned in the sequence protocol considering the degeneration of the genetic code.

For this purpose, hybridization or screening probes are used as DNA fragments, which generally comprise at least 15 nucleotides, typically between 15 and 30 nucleotides, and, if necessary, substantially more nucleotides. As an example, the primers employed in Example 1 may be used. Alternatively, DNA sequences of appropriate length, derived from the DNA sequences mentioned in the sequence protocol, may be used. As a third possibility, appropriate hybridization probes according to the invention may be developed starting from the amino acid sequences mentioned in the sequence protocol considering the degeneration of the genetic code.

In this respect, a subject-matter of the present invention are also genes encoding N-acetyl glucosaminyl transferase I, which may be detected from other varieties or plant species on account of the hybridization thereof to above mentioned hybridization probes, as well as DNA sequences, DNA fragments and constructs, which are derived therefrom in accordance with the above provisions.

The isolation of the corresponding gene and sequencing thereof following detection by means of the hybridization probes of the invention are well within the skills of a specialist in this field, and are detailed by way of example with respect to N-acetyl glucosaminyl transferase I from *Solanum tuberosum* and to the corresponding enzymes from *Nicotiana tabacum* and *Arabidopsis thaliana* (partial sequence) in the examples.

Finally, another subject matter of the present invention are antisense sequences with respect to any of the above DNA sequences.

iv) Constructs

Also comprised by the invention are constructs, which may optionally comprise besides additional 5' and/or 3' sequences, e.g. linkers and/or regulatory DNA sequences or other

modifications, the DNA sequences of the invention, including the DNA sequences derived as detailed above.

5 An example for this are hybridization or screening probes, which in addition to a DNA sequence of the invention also comprise a detection agent for the verification of hybridization products, which in this case typically is non-radioactive, e.g. fluorescent or phosphorescent molecules, 10 biotin, biotin derivatives, digoxigenin and digoxigenin derivatives. In this respect, however, radioactive or non-radioactive detection agents may be considered, which may be attached to the DNA sequence according to the present invention e.g. by means of end labelling. 15

A subject-matter of the invention are also antisense and sense constructs with respect to the DNA sequences and fragments according to the present invention, i.e. with respect to 20

- the DNA sequences mentioned in the sequence protocol and the corresponding genes;
- 25 - the DNA sequences derived therefrom in accordance with the above provisions;
- one or more regions of these DNA sequences;
- DNA sequences, especially from other varieties or plant species, which represent a gene or are a part of a gene, 30 encoding the enzyme N-acetyl glucosaminyl transferase I; and which hybridize under stringent conditions
 - to one or more of the above DNA sequences and/or
 - 35 -- to one or more of the above DNA fragments and/or
 - to a DNA sequence, which is derived from the amino acid sequences mentioned in the sequence protocol considering the degeneration of the 40 genetic code.

Furthermore, the present invention extends to any DNA-transfer systems such as vectors, plasmids, viral and phage genomes or cosmids, which contain the DNA sequences according

to the present invention, e.g. the *GntI* gene, cDNA and DNA regions according to the invention, as mentioned in the sequence protocol, fragments thereof, in particular antisense or sense constructs and/or cDNA sequences derived therefrom according to the above provisions.

Various techniques for the production or synthesis of DNA, DNA fragments, constructs and transfer systems according to the invention, e.g. digestion by means of restriction endonucleases, PCR amplification using suitable primers, optionally followed by cloning and additional chemical or enzymatic modification starting from plant DNA are well-known to those skilled in the art.

One possibility of application of the DNA hybridization probes according to the invention is the detection of N-acetyl glucosaminyl transferase I genes in plants other than those, from which the DNA sequences mentioned in the sequence protocol were obtained, or the detection of potential (other) isoforms of the N-acetyl glucosaminyl transferase I gene in the starting plants *Solanum tuberosum*, *Nicotiana tabacum* and *Arabidopsis thaliana*.

If it is possible to make use of a plant genomic library or cDNA library for the hybridization experiment, a positive hybridization result of such screening of each library may indicate a clone or a few clones, which contain the desired sequence completely or in part, i.e. the N-acetyl glucosaminyl transferase I gene, combined with only a limited amount of other DNA from the genome of the target plant, which appropriately facilitates cloning and sequencing of the target gene. As an alternative, a PCR amplification of the gene or parts thereof may also be carried out starting from plant DNA and suitable constructs, so-called PCR primers, to facilitate cloning and sequencing.

One use of sequencing primers of the invention, which are synthesized starting from suitable regions of the sequences according to the invention, e.g. enables genomic sequencing starting from the entire target plant genomic DNA cleaved by restriction endonucleases, by means of the Church-Gilbert technique, as well as sequencing at the cDNA level following RT-PCR amplification of the total RNA of the target plant (cf. Expl. 1).

An alternative possibility of application of the DNA hybridization probes according to the present invention derived from the DNA sequences mentioned in the sequence protocol, is the use thereof according to the invention for the detection of plants with reduced or lacking N-acetyl glucosaminyl transferase I activity. The hybridization experiment serves to detect the N-acetyl glucosaminyl transferase I (*GntI*) gene by which it may be concluded, e.g. owing to a negative hybridization result under stringent conditions, that the *GntI* gene, and thus, N-acetyl glucosaminyl transferase I activity in a plant investigated is lacking.

Such hybridization techniques for the detection of proteins or genes particularly in plant material by means of DNA probes are also known to the persons skilled in the art. In this context, it is referred to the above statements under item iii) for possible hybridization conditions. Generally, suitable DNA hybridization probes comprise at least 15 nucleotides of a sequence, which for example is derived from the cDNA sequences mentioned in Fig. 2 and the sequence protocol or from the corresponding *GntI* genes.

v) Transformed microorganisms

Furthermore, the invention relates to microorganisms, such as bacteria, bacteriophages, viruses, unicellular eukaryotic organisms, such as fungi, yeasts, protozoa, algae, and human, animal and plant cells, which have been transformed by one or

more of the DNA sequences of the invention or one or more of the constructs of the invention, as illustrated above.

Transformed microorganisms according to the present invention are used e.g. as expression systems for the transforming foreign DNA to obtain the corresponding expression products. For this purpose, typical microorganisms are bacteria, e.g. such as *E. coli*. Furthermore, transformed microorganisms according to the invention, in particular agrobacteria, may be employed e.g. for the transformation of plants by transmission of the transforming foreign DNA.

Methods for the transformation of cells of microorganisms by (foreign) DNA are well-known to those skilled in the art.

For this purpose, e.g. constructs referred to as expression vectors are used, which contain the DNA sequence of the invention under control of a constitutive or inducible promoter, which, if necessary, is additionally tissue specific, so as to enable the expression of the introduced DNA in the target or host cell.

Therefore, a further aspect of the invention is a method for the production of the enzymes and proteins of the invention by using one or more of the transformed microorganisms of the present invention. The method comprises cultivating at least one microorganism transformed by the DNA of the invention, in particular by one of the cDNAs mentioned in the sequence protocol, under the control of an active promoter, as defined above, and isolating the enzyme of the invention from the microorganisms, and, if applicable, also from the culture medium. It is understood, that this method also relates to the production of enzymes and proteins, respectively, which are derived from the enzymes according to the present invention from *Solanum tuberosum*, *Nicotiana tabacum* and *Arabidopsis thaliana*, as defined under i) above.

Methods for the cultivation of transformed microorganisms are well-known to those skilled in the art. For example, the isolation of the expressed enzyme may be employed according to the method described in Example 5 by means of metal-chelate chromatography or, alternatively, by chromatography via columns, which contain the antibodies against the enzyme bound to the packing material.

10 vi) Transgenic plants

Furthermore, the invention comprises transgenic plants, which are transformed by means of a DNA sequence according to the invention or a corresponding construct, respectively. Accordingly, there may be obtained e.g. transgenic plants, in which a GntI deficiency, for example on account of a missing or defective *GntI* gene or due to defects in the regulatory regions of this gene, has been removed by complementation using a construct derived from the cDNA sequences mentioned in the sequence protocol, wherein the expression of said construct is under the control of an active constitutive or inducible promoter, which may be additionally tissue specific. In this case, the GntI enzyme or protein expressed on account of the DNA of the invention contained in the construct and having GntI activity complements the GntI activity missing in the starting plant.

Also considered are transgenic plants, in which the GntI activity already present in the starting plant is increased by additional expression of the *GntI* transgene introduced by means of a construct according to the present invention. Up to now, the extremely low expression of the *GntI* gene *in vivo* accompanied by extremely low enzyme activity, which correspondingly was very difficult to detect, has been a main problem in the investigation of the enzyme N-acetyl glucosaminyl transferase I in plants. The problem of a too low GntI enzyme activity in plants may be overcome by the coexpression of a DNA according to the present invention.

In this case, it may be preferable for the transformation of plants to employ DNA according to the invention, additionally comprising a sequence region, which following expression enables a facilitated detection and/or enrichment and purification, respectively, of the protein product having GnTI activity. This is for example accomplished by the use of a specific DNA sequence for the expression of a recombinant GnTI enzyme, said sequence carrying a N-terminal or C-terminal sequence extension encoding an affinity marker. If it is additionally intended to provide an amino acid sequence portion between the GnTI enzyme and the affinity marker, which represents a recognition site for a specific protease, cleavage of the N-terminal or C-terminal sequence extension from the GnTI enzyme may be achieved by the subsequent use of this specific protease, and the GnTI enzyme thereby obtained in isolated form.

An example for this is the use of a DNA sequence according to the present invention, which codes for the recombinant GnTI enzyme with a C-terminal sequence extension, encoding the affinity marker AWRHPQFGG (strep-tag; ref. 39), and an intervening protease recognition site IEGR. The expression of the DNA according to the present invention provides GnTI enzymes with the C-terminal sequence extension mentioned, by means of which the expressed protein molecules specifically bind to a streptavidin derivatized matrix, and may thus be isolated. Then, by means of the protease factor Xa specifically recognizing the amino acid sequence IEGR, the GnTI portion of the protein molecules may be released. As an alternative, the complete protein may be removed from the streptavidin derivatized matrix by means of biotin or biotin derivatives.

A further example is represented by DNA sequences of the invention, encoding a protein which comprises multiple, e.g. 10, N-terminally added histidine residues (His-tag) in addition to a GnTI enzyme. Due to the N-terminal histidine residues, isola-

tion or purification, respectively, of the proteins expressed may be easily conducted by metal-chelate affinity chromatography (e.g. Ni sepharose) (cf. also Example 5).

5 Moreover, the invention comprises portions of such transgenic plants, adequately transformed plant cells, transgenic seeds and transgenic reproduction material.

10 A further important aspect of the invention is the use of the sequence information discussed above for the production of plants having reduced or lacking N-acetyl glucosaminyl transferase I activity.

15 The possibilities of identifying plants with reduced or lacking N-acetyl glucosaminyl transferase I activity due to a gene defect or a missing gene by means of antibodies of the invention or screening or hybridization probes of the inven-
20 tion have already been described above.

Two additional possibilities reside in the use according to
25 the invention of antisense or sense constructs, respectively, which are derived from the DNA sequence of a plant *GntI* gene, for the production of transgenic plants with reduced or lacking N-acetyl glucosaminyl transferase I activity by means of
30 homology-dependent gene silencing (cf. ref. 16,17). The DNA sequence used as a starting sequence for the generation of the constructs, may be derived from the starting plant to be transformed itself but also from a different plant variety or
35 species. In particular, antisense or sense constructs, as discussed under items iii) and iv) above are of use. Generally, the constructs employed comprise at least 50 to 200 and more base pairs.

40 In particular, the constructs employed for this purpose comprise at least 50 to 200 and more base pairs, with a sequence, which is derived on the basis of

- the cDNA sequences mentioned in the sequence protocol and/or the corresponding *GntI* genes and/or
- the derived DNA sequences discussed above and/or DNA fragments according to the present invention and/or
- 5 - the DNA sequences, in particular from other varieties and plant species, which encode N-acetyl glucosaminyl transferase I and which may be identified due to a hybridization under stringent conditions to hybridization or screening probes, as
- 10 defined under items iii) and iv) above.

Generally, the constructs contain a strong constitutive or inducible promoter, which additionally may be tissue specific, by means of which the antisense or sense DNA sequence regions are controlled.

In the production of transgenic plants by integration of antisense construct(s) into the plant genome or by viral infection of starting plants or plant cells by means of virus containing antisense construct(s) for an extrachomosomal propagation and transcription of the antisense construct or the antisense constructs in infected plant tissue, it is intended to achieve a hybridization of *GntI*-gene transcripts to transcripts of the antisense DNA region at the RNA level, which prevents translation of the *GntI* mRNA. The result is a transgenic plant with strongly decreased contents of N-acetyl glucosaminyl transferase I, and thus, a strongly decreased corresponding enzyme activity.

For the transformation of plants according to the invention with antisense constructs, for example constructs may be employed, which hybridize to one of the complete cDNAs, mentioned in Fig. 2 and in the sequence protocol, or to corresponding regions thereof, generally comprising at least 50 to more than 200 base pairs. Moreover, particularly preferred is the use of fragments, the transcripts of which additionally cause a hybridization to a portion of the 5' untranslated region of the *GntI* mRNA, at which or in the proximi-

mity of which usually the attachment of ribosomes would occur. Examples of such constructs are shown in Fig. 4.

5 In view of the occurrence of an isoform in *Solanum tuberosum*, which probably is located in the cytoplasm due to lack of the membrane anchor (aa 10 to 29) of yet unknown function, it may be desirable to target only the N-acetyl glucosaminyl transferase I enzyme located in the Golgi cisternae, i.e. only
10 that enzyme comprising the membrane anchor. One reason for this desire may be the effort or, in the individual case, also the requirement, to affect as little as possible the cytoplasmatic metabolism of the plant cell, for which the cytoplasmatic N-acetyl glucosaminyl transferase I possibly is
15 of importance. For this purpose, antisense constructs may be used according to the present invention, which themselves or the transcripts of which, respectively, hybridize to a DNA or
20 RNA region of the *GntI* gene or the *GntI* mRNA, comprising a part of the 5' untranslated region and the coding region including the membrane anchor. Generally, the extension of the region of hybridization up to position 266 of the cDNA in
25 Fig. 2 and SEQ ID NO: 1 is considered harmless for the purpose mentioned above.

30 In the production of transgenic plants by integration of sense constructs into the plant genome or by viral infection of starting plants or plant cells by means of virus containing sense construct(s) for extrachromosomal propagation and expression of the construct or constructs in infected plant tissue, there are
35 assumed hybridization phenomena in tobacco according to the work of Faske et al. (ref. 17), of said constructs to the endogenous *GntI* gene at a posttranscriptional or DNA level, respectively, which finally affect or prevent the translation of
40 the *GntI* gene. Also in this case, the result are transgenic plants having reduced or even lacking N-acetyl glucosaminyl transferase I activity.

Methods for the stable integration of such antisense and sense constructs into the genome of plants, or for the viral infection of plants or plant cells, respectively, for an extrachromosomal propagation and transcription/expression of such constructs in infected plant tissue are well known to those skilled in the art. This includes the direct DNA transfer (e.g. into protoplasts by means of electroporation or by the addition of a high molecular osmotic agent as well as biolistic methods, by which DNA coated particles are shot into the plant tissue), such as the use of natural host/vector systems (e.g. agrobacteria or plant viruses). For viral infection of starting plants or plant cells by viruses containing appropriate constructs for extrachromosomal propagation and transcription/expression of the constructs in infected plant tissue, a variety of specific viruses, such as tobacco mosaic virus (TMV) or potato virus X, is available.

Representative plants, which are suitable for such integration, comprise dicotyledonous as well as monocotyledonous cultivated plants, in particular *Solanaceae* such as potato, tobacco, tomato and pepper. Additionally, banana, alfalfa, canola, beets, soybean, lettuce, corn, rice and grain, would be suitable target plants for the use of homologous antisense constructs. For example, the sequence from *Arabidopsis thaliana* mentioned in the sequence protocol appears to be particularly suitable as a starting sequence for the transformation according to the invention of *Brassicaceae*, such as canola plants, by means of sense or antisense constructs. Further plants of interest are any plants, which express glycoproteins of interest for medicine and research.

Generally, it should be noted, that the transformation according to the invention of plants, which in the corresponding region of the *GntI* gene exhibit a homology of $\geq 70\%$ at the nucleotide level to the employed antisense or sense constructs according to the present invention, typically results in

transgenic plants of the invention, which show the desired reduction of N-acetyl glucosaminyl transferase I activity.

Further, another possibility is seen in the targeted destruction (knock-out) of the N-acetyl glucosaminyl transferase I gene via gene targeting by means of homologous recombination (ref. 24) in a target plant using a suitable DNA fragment derived from the cDNA sequence of the present invention, similar to the procedure established for yeast systems and mammals.

Further, the present invention comprises transgenic plants, which have been transformed by the antisense or sense constructs mentioned above or the viruses containing the same, respectively, as well as parts of such transgenic plants, correspondingly transformed plant cells, transgenic seeds and transgenic reproduction material.

Methods of the production of transgenic plants, e.g. by means of agrobacteria- or virus-mediated as well as direct DNA transfer are known to those skilled in the art. Concerning representative plants for such a transformation, the above mentioned applies.

The plants of the invention and the plants obtained according to the invention, respectively, with reduced or lacking N-acetyl glucosaminyl transferase I activity, may be used according to the invention for the production of glycoproteins with minimal and uniform, i.e. defined, sugar residues. As discussed above, such glycoproteins are of great importance for medicine and research. As a reasonable source of raw material and food as well as due to their unproblematical disposal via composting, plants per se represent ideal bioreactors. According to the present invention, it is now possible to express biotechnologically or pharmaceutically relevant glycoproteins (e.g. therapeutics of low antigenic

potential for mammals) in cultivated plants, in which GnTI activity is highly reduced or completely absent.

Accordingly, the invention also comprises a method for the production of glycoproteins with minimal uniform and defined sugar residues, comprising cultivating a transgenic plant according to the invention, of parts of such plants or of plant cells transformed according to the invention, each expressing the desired glycoprotein, as well as isolating the desired glycoprotein from the cultivated material.

In this context, representative cultivated plants are *Solanaceae*, in particular potato, tobacco, tomato and pepper. Furthermore possible are banana, alfalfa, canola, beets, soybean, lettuce, corn, rice and grain.

The sequence of the enzymatically controlled and plant specific N-glycan modifications, which secretory glycoproteins are subjected to during passage through the Golgi apparatus of higher plants, is schematically shown in Fig. 1. The biosynthesis block due to lacking or insufficient N-acetyl glucosaminyl transferase I (GlcNAc transferase I) activity in a plant leads, instead of complex glycans, to the predominant formation of glycans of the $\text{Man}_5\text{GlcNAc}_2$ type, i.e. glycoproteins with uniform and well-defined sugar residues, which are of extremely high importance for medicine and research.

For this purpose, the genes encoding the desired glycoproteins may be expressed in their natural producing plants, which have been transformed according to the present invention e.g. by means of antisense or sense constructs to yield transgenic plants with reduced or missing N-acetyl glucosaminyl transferase I activity.

There is also the possibility to use transgenic plants of the invention displaying reduced or lacking N-acetyl glucosaminyl transferase I activity, which additionally have been transformed by the gene encoding the desired glycoprotein. In order to achieve this, constructs may be employed, which contain the gene encoding the desired glycoprotein under the control of a strong constitutive or inducible promoter, which is optionally tissue specific as well, and lead to the integration of the gene into the plant genome. Alternatively, the transformation may also be conducted by viral infection by means of a virus containing the gene for the desired glycoprotein for extrachromosomal propagation and expression of the gene. The glycoprotein may then be expressed in the respective host plant and obtained therefrom.

Naturally, as an alternative, the procedure may be such, that initially a transformation using an expression construct or virus containing the DNA encoding the glycoprotein is performed, and subsequently, another transformation with one or more of the antisense or sense constructs of the invention or with one or more viruses, containing the corresponding DNA, is performed. It is also possible to perform a simultaneous transformation using both constructs or using one virus containing the antisense or sense construct as well as the gene encoding the desired glycoprotein (piggyback version).

Within the scope of the present invention, there is also considered a viral overinfection of the transgenic plants according to the invention, in which integration of an antisense/sense construct and/or the gene encoding the desired glycoprotein into the genome has already occurred, by viruses containing the antisense/sense construct and/or the gene encoding the desired glycoprotein, for an additional extrachromosomal propagation and transcription or expression, respectively, of this DNA. As a result, the concentrations of antisense or sense DNA, respectively; or of the expressed glycoprotein may be increased in the transgenic plant cells.

It may prove to be practical for the production according to the invention of glycoproteins with defined glycosylation, to use tissue specific promoters in such cases, where it is intended to obtain the desired glycoproteins specifically only from certain parts of a plant such as tubers or roots. Today, for a large variety of plant tissues, tissue specific promoters are available, which drive expression of foreign genes specifically only in these tissues. By way of example, tuber specific promoters such as patatin class I (ref. 26) and proteinase inhibitor II promoters (ref. 27) may be mentioned. Under certain conditions, both promoters exhibit expression also in leaf tissue, i.e. they can be induced by high metabolite contents (for example sucrose) and in the case of the proteinase inhibitor II promoter also by mechanical lesion or by spraying with abscisic or jasmonic acid, respectively.

The use of tissue specific promoters may also be indicated in cases, where the DNA sequence or the transcription products or translation products thereof according to the invention, respectively, which are employed for the transformation, turn out to be detrimental to certain plant parts, e.g. due to a negative influence on the metabolism of the corresponding plant cells.

As a representative target glycoprotein, human glucocerebrosidase may be used for the therapy of the hereditary Gaucher's disease (ref. 25). In order to obtain human glucocerebrosidase (GC) with uniform and defined sugar residues, e.g. plants of the present invention which are transformed by means of antisense DNA, may be transformed with the gene encoding human glucocerebrosidase. For this purpose, the human glucocerebrosidase cDNA sequence (ref. 38) is modified at the 3' terminus by means of PCR using gene specific primers in a manner, that the recombinant enzyme carries a C-terminal sequence extension encoding an affinity marker (e.g.

AWRHPQFGG, strep-tag; ref. 39) and, optionally, also a protease recognition site (e.g. IEGR) between the GntI enzyme region and the affinity marker. The GC-cDNA sequence thus altered is expressed in *GntI* antisense plants of the present invention by using a strong and optionally tissue specific promoter (e.g. for potato under the control of the tuber specific B33 patatin promoter), so that the enzyme synthesized in these plants exclusively carries well defined N-glycans. The affinity marker is intended to facilitate the enrichment of the recombinant enzyme from the transgenic plants. In this case, the expressed protein molecules (GC-strep molecules) bind to a streptavidin derivatized matrix via the affinity marker sequence and can be released therefrom by means of biotin or biotin derivatives. The removal from the streptavidin derivatized matrix may also be carried out by means of catalytic amounts of a protease, which exhibits a specificity for the protease recognition site located between the GntI enzyme region and the affinity marker. In this case, only the GntI enzyme region is released from the matrix. This could be advantageous especially in that case, if the affinity marker sequence has a detrimental effect on the GntI activity.

Due to their terminal mannose residues, the $\text{Man}_5\text{GlcNAc}_2$ -glycans of the glucocerebrosidase obtained from the plants of the present invention will be recognized by macrophages as an uptake signal, and can thus directly be employed for the therapy of hereditary Gaucher's disease. Currently, a therapy is only possible upon expensive isolation and deglycosylation of native glucocerebrosidase (ref. 25).

Accordingly, the production of recombinant glycoproteins may be highly facilitated by the use of plant *GntI* sequences compared to conventional methods, e.g. the chemical deglycosylation of purified glycoproteins, which is technically demanding (ref. 25), or a difficult and expensive production in GntI deficient animal cell lines (ref. 7,10).

Description of the figures:

Fig. 1: Sequence of plant specific N-glycan modifications, which secretory glycoproteins are subject to during passage through the Golgi apparatus of higher plants (ref. 28). The biosynthesis block to complex modified glycans is based on a deficiency in GnTI activity (which is either caused by a defective or missing GnTI enzyme or by effective reduction of the *GnTI* gene expression) and is indicated by a cross. Meaning of the symbols: (F) fucose residues, (X) xylose residues, (●) GlcNAc residues, (□) mannose residues.

Fig. 2: Full length cDNA sequence of a plant GnTI from potato (*Solanum tuberosum* L.) and amino acid sequence deduced therefrom. By way of example, the complete cDNA of the membrane anchor containing *GnTI* isoform from potato leaf tissue (A1) is illustrated. The EcoRI/NotI linkers at the 5' and 3' ends of the cDNA are highlighted by bold letters, the binding sites of the degenerate oligonucleotides used for obtaining the RT-PCR probe are underlined. In contrast to already published animal GnTI sequences, the protein sequence derived from the potato cDNA clones contains a potential N-glycosylation site: Asn-X(without Pro)-Ser/Thr, which is indicated by an asterisk. The region of the membrane anchor is highlighted in italics (aa 10 to 29). The start of the isoform (A8), which is potentially located in the cytosol, is indicated by an arrow.

Fig. 3: A, Degree of identity or similarity, respectively, of the amino acid sequence deduced from a complete *GnTI* cDNA sequence from potato (A1) in comparison to other GnTI sequences of animal organisms, which have been selected from data bases. Identical amino acid posi-

tions (in %) are printed in bold letters, similar amino acid positions are given in brackets underneath. Meaning of the abbreviations: Hu, human; Ra, rat; Mo, mouse; Ce, *Caenorhabditis elegans* (round-worm); St, *Solanum tuberosum* (potato).

B, Comparison of the derived amino acid sequences of different plant *GntI*-cDNA clones. A_Stb-A1, *GntI* from potato leaf; B_Ntb-A9, *GntI* from tobacco leaf (A9); C_Atb-Full, *GntI* from *Arabidopsis thaliana*. Identical aa are highlighted in black, similar aa in light grey.

Fig. 4: Cloning strategy of the *GntI*-antisense constructs used. Following fill-in of the ends, a *NotI* linker was introduced into the *SalI* restriction site of the polylinker region of the plant expression vector pA35 (=pA35N) (ref. 29), and the complete A1-*GntI*-cDNA was inserted into pA35N via *NotI*. The corresponding antisense construct (=pA35N-Alas) was inserted into binary vector pBin19 (ref. 30) via *EcoRI* and *HindIII*. Additionally, following PCR amplification, a 5' fragment of the A1-*GntI*-cDNA comprising 270 bp was cloned into pA35N via *XbaI* and *NotI* restriction sites in antisense orientation (=pA35N-A1-short) and also inserted into pBin19. Abbreviations; Numerals in brackets, positions of the restriction sites in the A1-*GntI*-cDNA (in base pairs); pBSK, cloning vector (Stratagene); pGEM3Z, cloning vector (Promega); CaMVp35S, constitutive 35S promoter of cauliflower mosaic virus; OCSpA, polyadenylation signal of octopine synthase; pNOS, promoter of nopaline synthase; NEO, neomycin phosphotransferase (selection marker, confers kanamycin resistance); NOSpA, polyadenylation signal of nopaline synthase; LB/RB, left/right border of the T-DNA of the binary vector; arrow, translation initiation (ATG); A8, start of the *GntI* isoform,

which is potentially located in the cytosol (7 aa substitutions in comparison to A1).

Fig. 5: Extent of suppression of complex glycoprotein modification in transgenic potato plants transformed with the long *GntI* antisense construct (cf. Fig. 4). A, Coomassie-stained SDS gel from leaf extracts; B, Western-blot analysis (Ref. 13,33) of parallel samples developed with a complex-glycan antiserum (Ref. 12,13). The lanes contain 30 µg each of total protein: *cgl*(Ara), Arabidopsis *cgl* mutant (Ref. 13); WT(Desi), wild-type potato; the numerals refer to individual transgenic potato plants; the arrows represent molecular weight standards of 66, 45, 36 and 29 kDa, respectively.

Fig. 6: Detection of specificity of the generated GntI antiserum following cell fractionation (Ref. 40) of tobacco callus material. For Western-blot analysis (Ref. 13,33) 30 µg of protein were applied per lane. The antiserum was used in 1:1000 dilution. Lane 1, homogenate following separation of cellular debris; lane 2, vesicle fraction following column chromatography; lane 3, sucrose gradient fraction I (microsomes); lane 4, sucrose gradient fraction II (plastids); lane 5, antigen used for immunization (recombinant GntI fusion protein); arrow, molecular weight of about 49 kDa.

Explanation of the abbreviations used in the text:

Aa, amino acid(s); bp, base pair(s); EMS, Ethyl methane sulfonate (mutagenic agent); F2, second filial generation; Fuc, fucose; Glc, glucose; GlcNAc, N-acetyl glucosamine; GntI, N-acetyl glucosaminyl transferase I (EC 2.4.1.101); *GntI*, gene for GntI (nuclear encoded); kDa, kilodalton; Man, mannose;

PCR, polymerase chain reaction; PAGE, polyacrylamide gel electrophoresis; ref., reference; RT-PCR, reverse transcription coupled polymerase chain reaction; SDS, sodium dodecyl sulfate; var., variety; Xyl, xylose.

In the following, the invention will be described in more detail by means of examples, which are only intended to illustrate the invention and shall not limit the invention in any manner.

Example 1

Isolation and characterization of plant *GntI* cDNA clones.

Total RNA was isolated from potato and tobacco leaf tissue, and cDNA fragments of about 90 bp were amplified by means of RT-PCR in combination with degenerate primers (procedure analogous to ref. 31), which were derived from conserved amino acid regions of known *GntI* sequences from animal organisms (sense primer 1*, 5'-TG(CT) G(CT)I (AT)(GC)I GCI TGG (AC)A(CT) GA(CT) AA(CT)-3'; antisense primer 3*, 5'-CCA ICC IT(AG) ICC (ACGT)G(CG) (AG)AA (AG)AA (AG)TC-3'; 30 pmol of each primer per 50 µl PCR assay at an annealing temperature of 55°C and 45 cycles). Following gel elution, the ends of the PCR products were repaired (i.e. blunt ended using DNA polymerase I and phosphorylated using T4 polynucleotide kinase) and cloned into the *EcoRV* restriction site of pBSK (Stratagene). By comparison with known *GntI* sequences between the primers (arrows), the identity of the derived amino acid sequences from the potato and tobacco RT-PCR products could be confirmed as being homologous; \Rightarrow Q(R/M)QFVQDP(D/Y)ALYRS \Leftarrow (homologous aa are underlined). Of one clone each, radio-labelled probes were synthesized by means of PCR (standard PCR assay using degenerate primers as above, nucleotide mixture without dCTP, but instead with 50 µCi α -³²P-dCTP [>3000 Ci/mMol]), and different cDNA libraries were screened for *GntI* containing clones using the corresponding homologous potato or tobacco probes, respectively (procedure analogous

to ref. 31; the stringent hybridization conditions have already been described in the text above). The cDNA libraries were prepared from mRNA of young and still growing plant parts (sink tissues). Following cDNA synthesis and ligating EcoRI/NotI adaptors (cDNA synthesis kit, Pharmacia) EcoRI compatible lambda arms were ligated, those packaged and used to transfect *E. coli* XL1 Blue cells (Lambda ZAPII cloning and packaging system, Stratagene). Following amplification of the libraries, one full-length *GntI* clone each was isolated from a potato leaf sink library (A1 according to Fig. 2 and SEQ ID NO: 1) and a tobacco leaf sink library (A9 according to SEQ ID NO: 3), as well as two additional clones from a tuber sink library (A6, A8). The deduced *GntI* amino-acid sequences contain a potential N-glycosylation site, Asn-X(without Pro)-Ser/Thr, in contrast to those of animals. One of the tuber *GntI* cDNA sequences carries stop codons in all three reading frames in front of the first methionine (A8). The coding region shows high homology to the longer tuber clone (A6) (only 2 aa substitutions), but displays a completely different 5' non-translated region. Furthermore, the membrane anchor characteristic for the Golgi enzyme is missing, so that this *GntI* isoform might be located in the cytosol. Sequence comparisons carried out by means of the gap or pileup option, respectively, and the box option of the gcg software package (J. Devereux, P. Haeberli, O. Smithies (1984) Nucl. Acids Res. 12: 387-395) indicate, that the deduced plant *GntI* amino-acid sequences exhibit only 30-40% identity and 57-59% similarity to those of animal organisms (Fig. 3A), while they are highly homologous among each other (75 - 90% identity, Fig. 3B).

The procedure in the case of *Arabidopsis thaliana* was analogous, wherein for the preparation of a specific probe first a partial *GntI* sequence was amplified by RT-PCR using *GntI* sense primer 4A (5'-ATCGGAAAGCTTGGATCC CCA GTG GC(AG) GCT GTA GTT GTT ATG GCT TGC-3'; HindIII restriction site underlined, BamHI printed in bold) and antisense primer 3*, as defined

above. First, a 5'-incomplete cDNA clone was isolated from a phage library (Lambda Uni-Zap) using this probe. By means of a vector insert PCR, the missing 5'-terminus was amplified from another library (via an unique SpeI restriction site in the 5' region) and assembled to yield a full-length cDNA sequence. The nucleic acid sequence determined by means of sequencing is listed in SEQ ID NO: 5.

Example 2

Functional complementation of a GntI defect using *GntI* cDNA upon transient expression in protoplasts of the *Arabidopsis thaliana* *cgl* mutant.

Approximately 4 weeks subsequent to sowing, protoplasts were isolated from leaves of *cgl* mutants cultivated under sterile conditions (nonstainer plants following 5 backcrosses, ref. 13), transformed with expression constructs of the complete *GntI* cDNA sequences (NotI cDNA fragments, cf. Fig. 4) in sense (pA35N-A1s or pA35N-A9s, respectively) or antisense orientation (pA35N-A1as or pA35N-A9as, respectively), and cultivated for 96 h at room temperature in the dark (50 µg of plasmid DNA each per 1 million protoplasts, PEG method according to ref. 32). Subsequent SDS-PAGE of the protoplast extracts and Western-blot analysis (analogous to ref. 13, 33) indicated functional complementation of the GntI defect, i.e. complex glycosylation of numerous protein bands upon transient expression of the potato A1 and tobacco A9 sense constructs, but not of the corresponding antisense constructs in protoplasts of the *Arabidopsis cgl* mutant (data not shown).

Example 3

Cloning of the binary expression constructs
pBin-35-Alas and pBin-35-Al-short (cf. Fig. 4).

5 Into the SalI restriction site of the polylinker region
(corresponding to the one of pUC18) of plant expression
vector pA35 (ref. 29), a NotI linker was introduced subse-
quently to the fill-in of the ends (=pA35N), and the complete
10 Al-*GntI*-cDNA (nucleotides 9 to 1657; according to the cDNA in
Fig. 2) was inserted into pA35N via NotI (sense construct
pA35N-Als and antisense construct pA35N-Alas, respectively).
The expression cassettes of the sense and antisense
15 constructs, respectively, were isolated via the terminal
restriction sites (filled-in NcoI restriction site, partial
post digestion with HindIII) as a fragment of about 2410 bp
and inserted into the EcoRI (filled-in) and HindIII
20 restriction sites of the binary vector pBin19 (Ref. 30)
(=pBin-35-Als and pBin-35-Alas, respectively). The EcoRI
restriction site of the vector is restored by fusion with the
equally filled-in NcoI restriction site of the fragment. By
25 means of a standard PCR assay (sense primer: KS sequencing
primer (Stratagene) extended for PCR, 5'-GGC CCC CCC TCG AGG
TCG ACG GTA TCG-3'; antisense primer: 5'-GGGCCTCTAGACTCGAG
AGC (CT)AC TAC TCT TCC TTG CTG CTG GCT AAT CTT G-3', XbaI
30 restriction site underlined, XhoI restriction site in ita-
lics), there was additionally amplified a 5'-fragment of the
GntI cDNA at an annealing temperature of 50°C (nucleotides 9
to 261, according to the cDNA in Fig. 2 and SEQ ID NO: 1).
35 The PCR product was digested with XbaI (within the antisense
primer) and NotI (within the 5'-linker of the cDNA), isolated
as a fragment of about 260 bp and cloned into pA35N (=pA35N-
Al-short). The expression cassette of the short antisense
40 construct was also inserted into pBin19 (=pBin-35-Al-short)
as a EcoRI/HindIII fragment (about 1020 bp).

Example 4

Transformation of agrobacteria by means of the binary *GntI* constructs and regeneration of transgenic potato and tobacco plants, respectively, from infected leaf discs.

5 The binary antisense *GntI* constructs (pBin-35-Alas and pBin-35-A1-short) were transformed into the Agrobacterium strain GV2260 (ref. 34, 35). By way of example, sterile leaf discs
10 of potato plants var. Désirée and of tobacco plants var. Wisconsin 38 were infected with the recombinant agrobacterial lines (50 µl of a fresh overnight culture in 10 ml liquid 2MS medium: 2% sucrose in Murashige & Skoog salt/vitamin standard
15 medium, pH 5.6; small pieces of leaf without midrip; co-cultivation for 2 days in the dark in phytotrons). Subsequent to washing of the infected leaf pieces in 2MS medium with 250 µg/ml claforan, transgenic plants were regenerated from said
20 pieces in tissue culture under kanamycin selection (potato protocol ref. 26; tobacco protocol ref. 36) and analyzed for reduced *GnTI* activity (exemplary shown in Fig. 5 for transgenic potato plants). As apparent from Fig. 5, antisense
25 suppression of complex glycoprotein modification was successful in transgenic potato plant #439. The determined reduction of complex glycoprotein modification was stable in this transformant over the entire investigation period of
30 several months and has been verified in three tests which were performed in an interval of about 1 month each. For the respective transgenic tobacco plants, analogous results were obtained.

Example 5

Production of recombinant potato *GnTI* protein
(for the production of antibodies).

40 Recombinant *GnTI* carrying 10 additional N-terminal histidine residues (His-tag) was produced in *E. coli* by means of the pET system (Novagen) and purified by metal-chelate affinity chromatography. A cDNA fragment comprising nucleotides 275-

1395 of the potato *GntI* cDNA (corresp. to aa 75-446, Fig. 2 and SEQ ID NO: 1 and 2, respectively) was amplified by standard PCR (annealing temperature of 50°C, 30 cycles, ref. 31) (sense primer *GntI*-5'fus: 5'-CATGGATCC CTC GAG AAG CGT CAG GAC CAG GAG TGC CGG C-3'; antisense primer *GntI*-3'stop: 5'-ATCCCGGGATCCG CTA CGT ATC TTC AAC TCC AAG TTG-3'; XhoI and BamHI restriction sites, respectively, are underlined, stop codon in italics), and inserted into vector pET16b (Novagen) (=pET-His-A1) via the restriction sites of the synthetic primer (5'-XhoI-*GntI*-BamHI-3'). Following propagation and analysis in *E. coli* XL1-Blue (Stratagene) the construct was stored as a glycerol culture. Competent *E. coli* BL21(DE3) pLysS cells (Novagen) were transformed with pET-His-A1 for overexpression. Addition of IPTG (Isopropyl-1-thio- β -D-galactopyranoside, at 0.5-2 mM) to a BL21 culture in logarithmic growth phase, initially induces the expression of T7 RNA polymerase (from the bacterial chromosome), and thus, also the expression of the recombinant fusion protein under control of the T7 promoter in pET vectors (Novagen). By means of metal-chelate chromatography using TALON matrix (Clontech), recombinant potato GntI was purified from induced BL21:pET-His-A1 cells under denaturing conditions via its His-tag (manufacturer's protocol, Novagen), and the preparation was verified with respect to homogeneity by means of SDS-PAGE.

Example 6

Raising of polyclonal antibodies in rabbits.

Recombinant potato GntI (from Expl. 5) was used as an antigen. Following the harvest of some milliliters of pre-immune serum, the rabbits were subcutaneously injected with 300-500 μ g of affinity-purified protein together with 25 μ g of GMDP adjuvant (Gerbu) in intervals of three weeks. Subsequent to three basis injections, the animals were bled from the ear vein 12 to 14 days after the respective successive injection (boost), the serum harvested (ref. 37) and tested for recognition of

recombinant GnTI by Western-blot analyses (dilution 1:200 to 1:2000). The antiserum of the boosts resulting in the lowest background-to-signal ratio were mixed with 0.04% sodium azide, aliquoted and kept at +4°C or for long-term storage at -20°C, respectively. As shown in Fig. 6, Western-blot analyses of tobacco callus cells (BY-2 suspension culture) revealed a specific GnTI signal in enriched microsomal fractions, which indicates, that antibodies raised against the recombinant protein specifically recognize plant GnTI. The detection was carried out with enriched microsomal fractions (ER and Golgi vesicles), since - due to low amounts - it is not possible to detect GnTI protein in crude plant extracts by means of the employed Western-blot method.

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tonoplast intrinsic protein are targeted to vacuoles in leaves of transgenic tobacco. *Planta* 184: 431-437

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assisted engineering of a C-terminal affinity peptide,
useful for the detection and purification of a functional
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endoplasmic reticulum of mung bean cotyledons: role in
the accumulation of hydrolases in protein bodies during
seedling growth. Plant Physiol. 66: 390-394

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: von Schaewen, Antje Dr. rer. nat.
 - (B) STREET: Natruperstrasse 169a
 - (C) CITY: Osnabrueck
 - (E) COUNTRY: Germany
 - (F) POSTAL CODE (ZIP): D-49076
 - (G) TELEPHONE: +49-541-684029
- (ii) TITLE OF INVENTION: Plant gntI sequences and the use thereof for the production of plants having reduced or lacking N-acetyl glucosaminyl transferase I (GnTI) activity
- (iii) NUMBER OF SEQUENCES: 6
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Solanum tuberosum
 - (B) STRAIN: Desiree
 - (D) DEVELOPMENTAL STAGE: Sink organ
 - (F) TISSUE TYPE: Mesophyll
 - (G) CELL TYPE: Leaf cells
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Lambda ZAP II (Eco RI)
 - (B) CLONE: gntI-A1(K)
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION: 659..667
 - (D) OTHER INFORMATION: /function= "Asn codon in this context is a potential glycosylation site"
/product= "N-glycosylation consensus sequence"
/phenotype= "N-glycans modulate protein properties"
/standard_name= "N-glycosylation site"
/label= pöt-CHO
/note= "GnTI-coding sequences from animals do not contain this feature"

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION:53..1393
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION:/codon_start= 53
 /function= "initiates complex N-glycans on
 secretory glycoproteins"
 /EC_number= 2.4.1.101
 /product=
 "beta-1,2-N-acetylglucosaminyltransferase I"
 /evidence= EXPERIMENTAL
 /gene= "cgl"
 /standard_name= "gntI"
 /label= ORF
 /note= "first gntI sequence from potato (unpublished)"

(ix) FEATURE:

(A) NAME/KEY: 5'UTR
 (B) LOCATION:15..52

(ix) FEATURE:

(A) NAME/KEY: 3'UTR
 (B) LOCATION:1394..1655

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION:80..139
 (D) OTHER INFORMATION:/function= "membrane anchor (amino
 acids 10-29)"
 /product= "hydrophobic amino acid stretch in GntI"
 /standard_name= "membrane anchor of a type II
 Golgi protein"
 /note= "identified by comparison with GntI sequences
 from animals"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION:1..14
 (D) OTHER INFORMATION:/function= "used for cloning the
 cDNA library in Lambda ZAPII"
 /product= "EcoRI/NotI-cDNA adapter"
 /number= 1

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION:1656..1669
 (D) OTHER INFORMATION:/product= "EcoRI/NotI-cDNA adapter"
 /number= 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCGCGG CCGCCTGAGA AACCCCTCGAA TTCAATTTTCG CATTGGCAG AG ATG	55
Met	
1	
AGA GGG AAC AAG TTT TGC TTT GAT TTA CGG TAC CTT CTC GTC GTG GCT	103
Arg Gly Asn Lys Phe Cys Phe Asp Leu Arg Tyr Leu Leu Val Val Ala	
5 10 15	
GCT CTC GCC TTC ATC TAC ATA CAG ATG CGG CTT TTC GCG ACA CAG TCA	151
Ala Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln Ser	

20	25	30	
GAA TAT GTA GAC CGC CTT GCT GCT GCA ATT GAA GCA GAA AAT CAT TGT Glu Tyr Val Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu Asn His Cys 35 40 45			199
ACA AGT CAG ACC AGA TTG CTT ATT GAC AAG ATT AGC CAG CAG CAA GGA Thr Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln Gly 50 55 60 65			247
AGA GTA GTA GCT CTT GAA GAA CAA ATG AAG CAT CAG GAC CAG GAG TGC Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu Cys 70 75 80			295
CGG CAA TTA AGG GCT CTT GTT CAG GAT CTT GAA AGT AAG GGC ATA AAA Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile Lys 85 90 95			343
AAG TTA ATC GGA GAT GTG CAG ATG CCA GTG GCA GCT GTA GTT GTT ATG Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val Met 100 105 110			391
GCT TGC AGT CGT ACT GAC TAC CTG GAG AGG ACT ATT AAA TCC ATC TTA Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile Leu 115 120 125			439
AAA TAC CAA ACA TCT GTT GCA TCA AAA TAT CCT CTT TTC ATA TCC CAG Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln 130 135 140 145			487
GAT GGA TCA AAT CCT GAT GTA AGA AAG CTT GCT TTG AGC TAT GGT CAG Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly Gln 150 155 160			535
CTG ACG TAT ATG CAG CAC TTG GAT TAT GAA CCT GTG CAT ACT GAA AGA Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu Arg 165 170 175			583
CCA GGG GAA CTG GTT GCA TAC TAC AAG ATT GCA CGT CAT TAC AAG TGG Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp 180 185 190			631
GCA TTG GAT CAG CTG TTT CAC AAG CAT AAT TTT AGC CGT GTT ATC ATA Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile Ile 195 200 205			679
CTA GAA GAT GAT ATG GAA ATT GCT GCT GAT TTT TTT GAC TAT TTT GAG Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe Glu 210 215 220 225			727
GCT GGA GCT ACT CTT CTT GAC AGA GAC AAG TCG ATT ATG GCT ATT TCT Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile Ser 230 235 240			775
TCT TGG AAT GAC AAT GGA CAA AGG CAG TTC GTC CAA GAT CCT GAT GCT Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp Ala 245 250 255			823

CTT TAC CGC TCA GAC TTT TTT CCT GGT CTT GGA TGG ATG CTT TCA AAA Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser Lys 260 265 270	871
TCA ACT TGG TCC GAA CTA TCT CCA AAG TGG CCA AAG GCT TAC TGG GAT Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp 275 280 285	919
GAC TGG CTA AGG CTG AAA GAA AAT CAC AGA GGT CGA CAA TTT ATT CGC Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile Arg 290 295 300 305	967
CCA GAA GTT TGC AGA ACG TAC AAT TTT GGT GAG CAT GGT TCT AGT TTG Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu 310 315 320	1015
GGG CAG TTT TTT AAG CAG TAT CTT GAG CCA ATT AAG CTA AAT GAT GTC Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val 325 330 335	1063
CAG GTT GAT TGG AAG TCA ATG GAC CTA AGT TAC CTT TTG GAG GAC AAC Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp Asn 340 345 350	1111
TAT GTG AAA CAC TTT GGC GAC TTG GTT AAA AAG GCT AAG CCC ATC CAC Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile His 355 360 365	1159
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ATT CAG TAC AGA GAC CAA CTA GAC TTT GAA GAT ATC GCT CGA CAG TTT Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe 390 395 400	1255
GGC ATT TTT GAA GAA TGG AAG GAT GGT GTA CCA CGG GCA GCA TAT AAA Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr Lys 405 410 415	1303
GGG ATA GTA GTT TTC CGG TTT CAA ACA TCT AGA CGT GTG TTC CTT GTT Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu Val 420 425 430	1351
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CGAAGATATG ATTGGAGCCT GAGCAACAAT TTAGACTTAT TTGGTAGGAT ACATTTGAAA	1453
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GGAACCCACT GCTTATTGTT GGAATGGATG AATCATCACC ACATCCTATT ATTCAAGTTT	1573
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GTTACGATTA TGAGCAACTT TGGCGGCCGC GAATTC	1669

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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20 25 30
Ser Glu Tyr Val Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu Asn His
35 40 45
Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln
50 55 60
Gly Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu
65 70 75 80
Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile
85 90 95
Lys Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val
100 105 110
Met Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile
115 120 125
Leu Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser
130 135 140
Gln Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly
145 150 155 160
Gln Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu
165 170 175
Arg Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys
180 185 190
Trp Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile
195 200 205
Ile Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe
210 215 220
Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile
225 230 235 240
Ser Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp
245 250 255
Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser
260 265 270

Lys	Ser	Thr	Trp	Ser	Glu	Leu	Ser	Pro	Lys	Trp	Pro	Lys	Ala	Tyr	Trp
	275						280					285			
Asp	Asp	Trp	Leu	Arg	Leu	Lys	Glu	Asn	His	Arg	Gly	Arg	Gln	Phe	Ile
	290					295					300				
Arg	Pro	Glu	Val	Cys	Arg	Thr	Tyr	Asn	Phe	Gly	Glu	His	Gly	Ser	Ser
305					310					315					320
Leu	Gly	Gln	Phe	Phe	Lys	Gln	Tyr	Leu	Glu	Pro	Ile	Lys	Leu	Asn	Asp
				325					330					335	
Val	Gln	Val	Asp	Trp	Lys	Ser	Met	Asp	Leu	Ser	Tyr	Leu	Leu	Glu	Asp
			340					345					350		
Asn	Tyr	Val	Lys	His	Phe	Gly	Asp	Leu	Val	Lys	Lys	Ala	Lys	Pro	Ile
		355					360					365			
His	Gly	Ala	Asp	Ala	Val	Leu	Lys	Ala	Phe	Asn	Ile	Asp	Gly	Asp	Val
	370					375					380				
Arg	Ile	Gln	Tyr	Arg	Asp	Gln	Leu	Asp	Phe	Glu	Asp	Ile	Ala	Arg	Gln
385					390					395					400
Phe	Gly	Ile	Phe	Glu	Glu	Trp	Lys	Asp	Gly	Val	Pro	Arg	Ala	Ala	Tyr
				405					410					415	
Lys	Gly	Ile	Val	Val	Phe	Arg	Phe	Gln	Thr	Ser	Arg	Arg	Val	Phe	Leu
			420					425					430		
Val	Ser	Pro	Asp	Ser	Leu	Arg	Gln	Leu	Gly	Val	Glu	Asp	Thr	*	
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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Nicotiana tabacum
- (B) STRAIN: Samsun NN
- (D) DEVELOPMENTAL STAGE: Sink organ
- (F) TISSUE TYPE: Mesophyll
- (G) CELL TYPE: Leaf cells

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Lambda ZAP II (Eco RI)
- (B) CLONE: gntI-A9(T)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:733..741
- (D) OTHER INFORMATION:/function= "Asn codon in this context is a potential glycosylation site"
/product= "N-glycosylation consensus sequence"
/phenotype= "N-glycans modulate protein properties"
/standard_name= "N-glycosylation site"
/label= pot-CHO
/note= "GnTI sequences from animals do not contain this feature"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:127..1467
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/codon_start= 127
/function= "initiates complex N-glycans on secretory glycoproteins"
/EC_number= 2.4.1.101
/product= "beta-1,2-N-acetylglucosaminyltransferase I"
/evidence= EXPERIMENTAL
/gene= "cgl"
/standard_name= "gntI"
/label= ORF
/note= "first gntI sequence from tobacco (unpublished)"

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION:15..126

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION:1468..1723

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:154..213
- (D) OTHER INFORMATION:/function= "membrane anchor (amino acids 10-29)"
/product= "hydrophobic amino acid stretch in GnTI"
/standard_name= "membrane anchor of a type II golgi protein"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..14
- (D) OTHER INFORMATION:/function= "use for cloning the cDNA library in Lambda ZAPII"
/product= "EcoRI/NotI-cDNA adapter"
/number= 1

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1724..1737
- (D) OTHER INFORMATION:/product= "EcoRI/NotI-cDNA adapter"
/number= 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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CGCACG ATG AGA GGG AAC AAG TTT TGC TGT GAT TTC CGG TAC CTC CTC	168
Met Arg Gly Asn Lys Phe Cys Cys Asp Phe Arg Tyr Leu Leu	
450 455 460	
ATC TTG GCT GCT GTC GCC TTC ATC TAC ACA CAG ATG CGG CTT TTT GCG	216
Ile Leu Ala Ala Val Ala Phe Ile Tyr Thr Gln Met Arg Leu Phe Ala	
465 470 475	
ACA CAG TCA GAA TAT GCA GAT CGC CTT GCT GCT GCA ATT GAA GCA GAA	264
Thr Gln Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu	
480 485 490	
AAT CAT TGT ACA AGC CAG ACC AGA TTG CTT ATT GAC CAG ATT AGC CTG	312
Asn His Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Gln Ile Ser Leu	
495 500 505	
CAG CAA GGA AGA ATA GTT GCT CTT GAA GAA CAA ATG AAG CGT CAG GAC	360
Gln Gln Gly Arg Ile Val Ala Leu Glu Glu Gln Met Lys Arg Gln Asp	
510 515 520 525	
CAG GAG TGC CGA CAA TTA AGG GCT CTT GTT CAG GAT CTT GAA AGT AAG	408
Gln Glu Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys	
530 535 540	
GGC ATA AAA AAG TTG ATC GGA AAT GTA CAG ATG CCA GTG GCT GCT GTA	456
Gly Ile Lys Lys Leu Ile Gly Asn Val Gln Met Pro Val Ala Ala Val	
545 550 555	
GTT GTT ATG GCT TGC AAT CGG GCT GAT TAC CTG GAA AAG ACT ATT AAA	504
Val Val Met Ala Cys Asn Arg Ala Asp Tyr Leu Glu Lys Thr Ile Lys	
560 565 570	
TCC ATC TTA AAA TAC CAA ATA TCT GTT GCG TCA AAA TAT CCT CTT TTC	552
Ser Ile Leu Lys Tyr Gln Ile Ser Val Ala Ser Lys Tyr Pro Leu Phe	
575 580 585	
ATA TCC CAG GAT GGA TCA CAT CCT GAT GTC AGG AAG CTT GCT TTG AGC	600
Ile Ser Gln Asp Gly Ser His Pro Asp Val Arg Lys Leu Ala Leu Ser	
590 595 600 605	
TAT GAT CAG CTG ACG TAT ATG CAG CAC TTG GAT TTT GAA CCT GTG CAT	648
Tyr Asp Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val His	
610 615 620	
ACT GAA AGA CCA GGG GAG CTG ATT GCA TAC TAC AAA ATT GCA CGT CAT	696
Thr Glu Arg Pro Gly Glu Leu Ile Ala Tyr Tyr Lys Ile Ala Arg His	
625 630 635	
TAC AAG TGG GCA TTG GAT CAG CTG TTT TAC AAG CAT AAT TTT AGC CGT	744
Tyr Lys Trp Ala Leu Asp Gln Leu Phe Tyr Lys His Asn Phe Ser Arg	
640 645 650	
GTT ATC ATA CTA GAA GAT GAT ATG GAA ATT GCC CCT GAT TTT TTT GAC	792
Val Ile Ile Leu Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp	
655 660 665	
TTT TTT GAG GCT GGA GCT ACT CTT CTT GAC AGA GAC AAG TCG ATT ATG	840

Phe	Phe	Glu	Ala	Gly	Ala	Thr	Leu	Leu	Asp	Arg	Asp	Lys	Ser	Ile	Met	
670					675					680					685	
GCT	ATT	TCT	TCT	TGG	AAT	GAC	AAT	GGA	CAA	ATG	CAG	TTT	GTC	CAA	GAT	888
Ala	Ile	Ser	Ser	Trp	Asn	Asp	Asn	Gly	Gln	Met	Gln	Phe	Val	Gln	Asp	
				690					695					700		
CCT	TAT	GCT	CTT	TAC	CGC	TCA	GAT	TTT	TTT	CCC	GGT	CTT	GGA	TGG	ATG	936
Pro	Tyr	Ala	Leu	Tyr	Arg	Ser	Asp	Phe	Phe	Pro	Gly	Leu	Gly	Trp	Met	
			705					710					715			
CTT	TCA	AAA	TCT	ACT	TGG	GAC	GAA	TTA	TCT	CCA	AAG	TGG	CCA	AAG	GCT	984
Leu	Ser	Lys	Ser	Thr	Trp	Asp	Glu	Leu	Ser	Pro	Lys	Trp	Pro	Lys	Ala	
		720					725					730				
TAC	TGG	GAC	GAC	TGG	CTA	AGA	CTC	AAA	GAG	AAT	CAC	AGA	GGT	CGA	CAA	1032
Tyr	Trp	Asp	Asp	Trp	Leu	Arg	Leu	Lys	Glu	Asn	His	Arg	Gly	Arg	Gln	
	735					740					745					
TTT	ATT	CGC	CCA	GAA	GTT	TGC	AGA	ACA	TAT	AAT	TTT	GGT	GAG	CAT	GGT	1080
Phe	Ile	Arg	Pro	Glu	Val	Cys	Arg	Thr	Tyr	Asn	Phe	Gly	Glu	His	Gly	
750					755					760					765	
TCT	AGT	TTG	GGG	CAG	TTT	TTC	AAG	CAG	TAT	CTT	GAG	CCA	ATT	AAA	CTA	1128
Ser	Ser	Leu	Gly	Gln	Phe	Phe	Lys	Gln	Tyr	Leu	Glu	Pro	Ile	Lys	Leu	
				770					775					780		
AAT	GAT	GTC	CAG	GTT	GAT	TGG	AAG	TCA	ATG	GAC	CTT	AGT	TAC	CTT	TTG	1176
Asn	Asp	Val	Gln	Val	Asp	Trp	Lys	Ser	Met	Asp	Leu	Ser	Tyr	Leu	Leu	
			785					790					795			
GAG	GAC	AAT	TAC	GTG	AAA	CAC	TTT	GGT	GAC	TTG	GTT	AAA	AAG	GCT	AAG	1224
Glu	Asp	Asn	Tyr	Val	Lys	His	Phe	Gly	Asp	Leu	Val	Lys	Lys	Ala	Lys	
		800					805					810				
CCC	ATC	CAT	GGA	GCT	GAT	GCT	GTC	TTG	AAA	GCA	TTT	AAC	ATA	GAT	GGT	1272
Pro	Ile	His	Gly	Ala	Asp	Ala	Val	Leu	Lys	Ala	Phe	Asn	Ile	Asp	Gly	
	815					820					825					
GAT	GTG	CGT	ATT	CAG	TAC	AGA	GAT	CAA	CTA	GAC	TTT	GAA	AAT	ATC	GCA	1320
Asp	Val	Arg	Ile	Gln	Tyr	Arg	Asp	Gln	Leu	Asp	Phe	Glu	Asn	Ile	Ala	
830					835					840					845	
CGG	CAA	TTT	GGC	ATT	TTT	GAA	GAA	TGG	AAG	GAT	GGT	GTA	CCA	CGT	GCA	1368
Arg	Gln	Phe	Gly	Ile	Phe	Glu	Glu	Trp	Lys	Asp	Gly	Val	Pro	Arg	Ala	
				850					855					860		
GCA	TAT	AAA	GGA	ATA	GTA	GTT	TTC	CGG	TAC	CAA	ACG	TCC	AGA	CGT	GTA	1416
Ala	Tyr	Lys	Gly	Ile	Val	Val	Phe	Arg	Tyr	Gln	Thr	Ser	Arg	Arg	Val	
			865					870					875			
TTC	CTT	GTT	GGC	CAT	GAT	TCG	CTT	CAA	CAA	CTC	GGA	ATT	GAA	GAT	ACT	1464
Phe																

CATCAACACA ACCTATTATT TTAAGTGTTT AGAACATAAA GAGGAAATGT AGCCCTGTAA 1697
AGACTATACA TGGGACCATC ATAATCGCGG CCGCGAATTC 1737

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Arg Gly Asn Lys Phe Cys Cys Asp Phe Arg Tyr Leu Leu Ile Leu
1 5 10 15
Ala Ala Val Ala Phe Ile Tyr Thr Gln Met Arg Leu Phe Ala Thr Gln
20 25 30
Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu Asn His
35 40 45
Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Gln Ile Ser Leu Gln Gln
50 55 60
Gly Arg Ile Val Ala Leu Glu Glu Gln Met Lys Arg Gln Asp Gln Glu
65 70 75 80
Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile
85 90 95
Lys Lys Leu Ile Gly Asn Val Gln Met Pro Val Ala Ala Val Val Val
100 105 110
Met Ala Cys Asn Arg Ala Asp Tyr Leu Glu Lys Thr Ile Lys Ser Ile
115 120 125
Leu Lys Tyr Gln Ile Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser
130 135 140
Gln Asp Gly Ser His Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Asp
145 150 155 160
Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val His Thr Glu
165 170 175
Arg Pro Gly Glu Leu Ile Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys
180 185 190
Trp Ala Leu Asp Gln Leu Phe Tyr Lys His Asn Phe Ser Arg Val Ile
195 200 205
Ile Leu Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Phe Phe
210 215 220
Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile
225 230 235 240
Ser Ser Trp Asn Asp Asn Gly Gln Met Gln Phe Val Gln Asp Pro Tyr
245 250 255

Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser
 260 265 270

Lys Ser Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp
 275 280 285

Asp Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile
 290 295 300

Arg Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser
 305 310 315 320

Leu Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp
 325 330 335

Val Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp
 340 345 350

Asn Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile
 355 360 365

His Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val
 370 375 380

Arg Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asn Ile Ala Arg Gln
 385 390 395 400

Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr
 405 410 415

Lys Gly Ile Val Val Phe Arg Tyr Gln Thr Ser Arg Arg Val Phe Leu
 420 425 430

Val Gly His Asp Ser Leu Gln Gln Leu Gly Ile Glu Asp Thr *

435 440 445

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1854 base pairs
 - (B) TYPE: Nucleotide
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: Columbia
 - (D) DEVELOPMENTAL STAGE: Mature plants
 - (F) TISSUE TYPE: All tissues
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Lambda Uni-ZAP (EcoRI/XhoI) and
 Lambda ACT (XhoI)
 - (B) CLONE: pBSK-Ara-GntI-full #8
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1185..1193
- (D) OTHER INFORMATION:/function= "Asn Codon is a potential glycosylation site"
/product= "Consensus sequence for N-glycosylation"
/phenotype= "N glycans modulate protein characteristics"
/standard_name= "N glycosylation site"
/label= pot-CHO
/note= "absent in animal GnTI sequences"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:135..1469
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/codon_start= 135
/function= "initiates complex N glycans on secretory glycoproteins"
/EC_number= 2.4.1.101
/product= "beta-1,2-N-acetyl glucosaminyl transferase I"
/evidence= EXPERIMENTAL
/gene= "cgl"
/standard_name= "gntI"
/label= ORF
/note= "first gntI sequence from Arabidopsis (unpublished)"

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION:19..134

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION:1470..1848

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:157..215
- (D) OTHER INFORMATION:/function= "membrane anchor (amino acids 8-27)"
/product= "hydrophobic amino-acid region in GnTI"
/standard_name= "membrane anchor of a Type II Golgi protein"
/note= "identified by comparison with animal GnTI sequences "

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..18
- (D) OTHER INFORMATION:/function= "for preparation of a cDNA library in Lambda ACT"
/product= "XhoI-cDNA-Adaptor"
/number= 1

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1849..1854
- (D) OTHER INFORMATION:/product= "XhoI-cDNA-Adaptor"
/number= 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTCGAGGCCA CGAAGGCCAC CGTTTTTGTT ATAACGAACG ACACCGTTTC AAACAAC TTC	60
CTTATTAGCT AGCTCCCTCC CGGCGGCAAA CACCAGAAGA TCCACCGCTT TTGATCTGGT	120
TGTTTGTCGT CGAT ATG GCG AGG ATC TCG TGT GAC TTG AGA TTT CTT CTC	170
Met Ala Arg Ile Ser Cys Asp Leu Arg Phe Leu Leu	
1 5 10	
ATC CCG GCA GCT TTC ATG TTC ATC TAC ATC CAG ATG AGG CTT TTC CAG	218
Ile Pro Ala Ala Phe Met Phe Ile Tyr Ile Gln Met Arg Leu Phe Gln	
15 20 25	
ACG CAA TCA CAG TAT GCA GAT CGC CTC AGT TCC GCT ATC GAA TCT GAG	266
Thr Gln Ser Gln Tyr Ala Asp Arg Leu Ser Ser Ala Ile Glu Ser Glu	
30 35 40	
AAC CAT TGC ACT AGT CAA ATG CGA GGC CTC ATA GAT GAA GTT AGC ATC	314
Asn His Cys Thr Ser Gln Met Arg Gly Leu Ile Asp Glu Val Ser Ile	
45 50 55 60	
AAA CAG TCG CGG ATT GTT GCC CTC GAA GAT ATG AAG AAC CGC CAG GAC	362
Lys Gln Ser Arg Ile Val Ala Leu Glu Asp Met Lys Asn Arg Gln Asp	
65 70 75	
GAA GAA CTT GTG CAG CTT AAG GAT CTA ATC CAG ACG TTT GAA AAA AAA	410
Glu Glu Leu Val Gln Leu Lys Asp Leu Ile Gln Thr Phe Glu Lys Lys	
80 85 90	
GGA ATA GCA AAA CTC ACT CAA GGT GGA CAG ATG CCT GTG GCT GCT GTA	458
Gly Ile Ala Lys Leu Thr Gln Gly Gly Gln Met Pro Val Ala Ala Val	
95 100 105	
GTG GTT ATG GCC TGC AGT CGT GCA GAC TAT CTT GAA AGG ACT GTT AAA	506
Val Val Met Ala Cys Ser Arg Ala Asp Tyr Leu Glu Arg Thr Val Lys	
110 115 120	
TCA GTT TTA ACA TAT CAA ACT CCC GTT GCT TCA AAA TAT CCT CTA TTT	554
Ser Val Leu Thr Tyr Gln Thr Pro Val Ala Ser Lys Tyr Pro Leu Phe	
125 130 135 140	
ATA TCT CAG GAT GGA TCT GAT CAA GCT GTC AAG AGC AAG TCA TTG AGC	602
Ile Ser Gln Asp Gly Ser Asp Gln Ala Val Lys Ser Lys Ser Leu Ser	
145 150 155	
TAT AAT CAA TTA ACA TAT ATG CAG CAC TTG GAT TTT GAA CCA GTG GTC	650
Tyr Asn Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val Val	
160 165 170	
ACT GAA AGG CCT GGT GAA CTG ACT GCG TAC TAC AAG ATT GCA CGT CAC	698
Thr Glu Arg Pro Gly Glu Leu Thr Ala Tyr Tyr Lys Ile Ala Arg His	
175 180 185	
TAC AAG TGG GCA CTG GAC CAG TTG TTT TAC AAA CAC AAA TTT AGT CGA	746
Tyr Lys Trp Ala Leu Asp Gln Leu Phe Tyr Lys His Lys Phe Ser Arg	
190 195 200	
GTG ATT ATA CTA GAA GAC GAT ATG GAA ATT GCT CCA GAC TTC TTT GAT	794
Val Ile Ile Leu Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp	
205 210 215 220	

TTGAAAGGGT CAGGGTTAAA TATATTTTCAG TTGTTTTATT AGTGATTATC TTGTGGGTAA 1699
 CTTATACGAA TGCAAATCAT TCTATGCAGT TTTTCTTCGT CCCACTTGTT TTGGCTTCTC 1759
 TATTGCTAGT GTACATATCT CTTCAAACAT GACTAAATA ATGCGTGTTG CTTCAAAGAA 1819
 GTAACTTTTA TTAACAAAAA AAAAAAAAC TCGAG 1854

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 amino acids
 (B) TYPE: Amino acid
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Arg Ile Ser Cys Asp Leu Arg Phe Leu Leu Ile Pro Ala Ala
 1 5 10 15
 Phe Met Phe Ile Tyr Ile Gln Met Arg Leu Phe Gln Thr Gln Ser Gln
 20 25 30
 Tyr Ala Asp Arg Leu Ser Ser Ala Ile Glu Ser Glu Asn His Cys Thr
 35 40 45
 Ser Gln Met Arg Gly Leu Ile Asp Glu Val Ser Ile Lys Gln Ser Arg
 50 55 60
 Ile Val Ala Leu Glu Asp Met Lys Asn Arg Gln Asp Glu Glu Leu Val
 65 70 75 80
 Gln Leu Lys Asp Leu Ile Gln Thr Phe Glu Lys Lys Gly Ile Ala Lys
 85 90 95
 Leu Thr Gln Gly Gly Gln Met Pro Val Ala Ala Val Val Val Met Ala
 100 105 110
 Cys Ser Arg Ala Asp Tyr Leu Glu Arg Thr Val Lys Ser Val Leu Thr
 115 120 125
 Tyr Gln Thr Pro Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln Asp
 130 135 140
 Gly Ser Asp Gln Ala Val Lys Ser Lys Ser Leu Ser Tyr Asn Gln Leu
 145 150 155 160
 Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val Val Thr Glu Arg Pro
 165 170 175
 Gly Glu Leu Thr Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp Ala
 180 185 190
 Leu Asp Gln Leu Phe Tyr Lys His Lys Phe Ser Arg Val Ile Ile Leu
 195 200 205
 Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Tyr Phe Glu Ala
 210 215 220
 Ala Ala Ser Leu Met Asp Arg Asp Lys Thr Ile Met Ala Ala Ser Ser

225		230		235		240
Trp Asn Asp Asn Gly Gln Lys Gln Phe Val His Asp Pro Tyr Ala Leu						
	245			250		255
Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Lys Arg Ser						
	260			265		270
Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp Asp						
	275			280		285
Trp Leu Arg Leu Lys Glu Asn His Lys Gly Arg Gln Phe Ile Ala Pro						
	290			295		300
Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu Gly						
	305			310		315
Gln Phe Phe Ser Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val Thr						
	325			330		335
Val Asp Trp Lys Ala Lys Asp Leu Gly Tyr Leu Thr Glu Gly Asn Tyr						
	340			345		350
Thr Lys Tyr Phe Ser Gly Leu Val Arg Gln Ala Arg Pro Ile Gln Gly						
	355			360		365
Ser Asp Leu Val Leu Lys Ala Gln Asn Ile Lys Asp Asp Asp Arg Ile						
	370			375		380
Arg Tyr Lys Asp Gln Val Glu Phe Glu Arg Ile Ala Gly Glu Phe Gly						
	385			390		395
Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Thr Ala Tyr Lys Gly						
	405			410		415
Val Val Val Phe Arg Ile Gln Thr Thr Arg Arg Val Phe Leu Val Gly						
	420			425		430
Pro Asp Ser Val Met Gln Leu Gly Ile Arg Asn Ser *						
	435			440		445